

SEQUENCE LISTING

<110> MARINE BIOTECHNOLOGY INSTITUTE CO., LTD.

<120> METHOD FOR IDENTIFICATION AND DETECTION OF MICROORGANISMS USING GYRASE GENE AS
AN INDICATOR

<130> PH-581

<140> US09/208,688

<141> 1998-12-10

<150> JP97/343316

<151> 1997-12-12

<160> 80

<170> PatentIn version 2.0

<210> 1

<211> 1212

<212> DNA

<213> Bacteroides vulgatus

<220>

<221> CDS

<222> (1)... (1212)

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Ser	Cys	Val	Asn	Ala	Leu	Ser	Thr	His	Met	Thr	Thr	Gln	Val	Phe	Arg	
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Gly	Gly	Lys	Ile	Tyr	Gln	Gln	Glu	Tyr	Ser	Cys	Gly	His	Pro	Leu	Tyr	
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tct	gta	aaa	gaa	gta	gga	aca	gct	gat	att	acc	gga	aca	aaa	cag	act	192
Ser	Val	Lys	Glu	Val	Gly	Thr	Ala	Asp	Ile	Thr	Gly	Thr	Lys	Gln	Thr	
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Phe	Trp	Pro	Asp	Asp	Thr	Ile	Phe	Thr	Val	Thr	Glu	Tyr	Lys	Phe	Asp	
65				70					75				80			
att	cta	cag	gca	cgt	atg	cgt	gaa	tgg	gcc	tac	ttg	aac	aaa	ggt	atc	288
Ile	Leu	Gln	Ala	Arg	Met	Arg	Glu	Leu	Ala	Tyr	Leu	Asn	Lys	Gly	Ile	
		85					90					95				
acc	att	tca	ctg	acc	gac	cgc	cgg	atc	aaa	gaa	gaa	gat	ggc	agc	ttc	336
Thr	Ile	Ser	Leu	Thr	Asp	Arg	Arg	Ile	Lys	Glu	Glu	Asp	Gly	Ser	Phe	
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aag	aaa	gaa	ata	ttc	cat	tcg	gac	gaa	gga	gtg	aaa	gag	ttt	gta	cgt	384
Lys	Lys	Glu	Ile	Phe	His	Ser	Asp	Glu	Gly	Val	Lys	Glu	Phe	Val	Arg	
	115					120				125						
ttc	ctg	aac	cgt	aac	aac	gaa	cgc	ctg	att	aat	gat	gtc	att	tat	ctg	432
Phe	Leu	Asn	Arg	Asn	Asn	Glu	Ala	Leu	Ile	Asn	Asp	Val	Ile	Tyr	Leu	
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Asn	Thr	Glu	Lys	Asn	Asn	Thr	Pro	Ile	Glu	Cys	Ala	Ile	Met	Tyr	Asn	

145	150	155	160	
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Thr Gly Tyr Arg Glu Ser Leu His Ser Tyr Val Asn Asn Ile Asn Thr				
165	170	175		
ata gaa ggc ggt aca cac gag gcc ggt ttc cgc agc gca tta acc cgt				576
Ile Glu Gly Gly Thr His Glu Ala Gly Phe Arg Ser Ala Leu Thr Arg				
180	185	190		
gta ctg aag aaa tat gcg gaa gat acc aaa gca ctg gaa aaa gca aaa				624
Val Leu Lys Lys Tyr Ala Glu Asp Thr Lys Ala Leu Glu Lys Ala Lys				
195	200	205		
gtc gag att tcg gga gag gac ttc cgc gaa ggc ttg att gcc gtc att				672
Val Glu Ile Ser Gly Glu Asp Phe Arg Glu Gly Leu Ile Ala Val Ile				
210	215	220		
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Ser Val Lys Val Ala Glu Pro Gln Phe Glu Gly Gln Thr Lys Thr Lys				
225	230	235	240	
ctg ggc aac agc gaa gtg agt ggt gcc gtg aac caa gct gta ggc gaa				768
Leu Gly Asn Ser Glu Val Ser Gly Ala Val Asn Gln Ala Val Gly Glu				
245	250	255		
gcg ctt aca tat tat ctg gaa gaa cat ccg aaa gaa gca aaa cag att				816
Ala Leu Thr Tyr Tyr Leu Glu Glu His Pro Lys Glu Ala Lys Gln Ile				
260	265	270		
gtt gac aaa gtg atc ctg gct gca aca gcg cgt atc gcc gca cgc aag				864
Val Asp Lys Val Ile Leu Ala Ala Thr Ala Arg Ile Ala Ala Arg Lys				
275	280	285		
gca cgt gaa tct gtt caa aga aag agt ccg atg ggc ggt ggc gga ctg				912
Ala Arg Glu Ser Val Gln Arg Lys Ser Pro Met Gly Gly Gly Gly Leu				
290	295	300		
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Pro Gly Lys Leu Ala Asp Cys Ser Ser Arg Asn Pro Glu Glu Cys Glu
 305 310 315 320
 cta ttc ctg gtc gag ggt gac tcg gca ggt ggt tct gcc aag caa gga 1008
 Leu Phe Leu Val Glu Gly Asp Ser Ala Gly Gly Ser Ala Lys Gln Gly
 325 330 335
 cgt agc cgt gcc ttc cag gca att cta cct ttg agg ggt aaa atc ctg 1056
 Arg Ser Arg Ala Phe Gln Ala Ile Leu Pro Leu Arg Gly Lys Ile Leu
 340 345 350
 aat gtg gaa aaa gcg atg tgg cac aag gct ttt gaa agc gat gag gtc 1104
 Asn Val Glu Lys Ala Met Trp His Lys Ala Phe Glu Ser Asp Glu Val
 355 360 365
 aat aat atc atc acc gcc ctg ggt gtc cgt ttc ggt gtg gac gga aat 1152
 Asn Asn Ile Ile Thr Ala Leu Gly Val Arg Phe Gly Val Asp Gly Asn
 370 375 380
 gat gac agc aaa aaa gcg aac atc gac aag ctg cgt tat cac aaa gtg 1200
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 Val Ile Met Thr

<210> 2

<211> 404

<212> PRT

<213> Bacteroides vulgatus

<400> 2

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Ser	Val	Lys	Glu	Val	Gly	Thr	Ala	Asp	Ile	Thr	Gly	Thr	Lys	Gln	Thr	
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Phe	Trp	Pro	Asp	Asp	Thr	Ile	Phe	Thr	Val	Thr	Glu	Tyr	Lys	Phe	Asp	
65					70					75					80	
Ile	Leu	Gln	Ala	Arg	Met	Arg	Glu	Leu	Ala	Tyr	Leu	Asn	Lys	Gly	Ile	
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Thr	Ile	Ser	Leu	Thr	Asp	Arg	Arg	Ile	Lys	Glu	Glu	Asp	Gly	Ser	Phe	
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Lys	Lys	Glu	Ile	Phe	His	Ser	Asp	Glu	Gly	Val	Lys	Glu	Phe	Val	Arg	
115					120					125						
Phe	Leu	Asn	Arg	Asn	Asn	Glu	Ala	Leu	Ile	Asn	Asp	Val	Ile	Tyr	Leu	
130					135					140						
Asn	Thr	Glu	Lys	Asn	Asn	Thr	Pro	Ile	Glu	Cys	Ala	Ile	Met	Tyr	Asn	
145					150					155					160	
Thr	Gly	Tyr	Arg	Glu	Ser	Leu	His	Ser	Tyr	Val	Asn	Asn	Ile	Asn	Thr	
165					170					175						
Ile	Glu	Gly	Gly	Thr	His	Glu	Ala	Gly	Phe	Arg	Ser	Ala	Leu	Thr	Arg	
180					185					190						
Val	Leu	Lys	Lys	Tyr	Ala	Glu	Asp	Thr	Lys	Ala	Leu	Glu	Lys	Ala	Lys	
195					200					205						
Val	Glu	Ile	Ser	Gly	Glu	Asp	Phe	Arg	Glu	Gly	Leu	Ile	Ala	Val	Ile	
210					215					220						
Ser	Val	Lys	Val	Ala	Glu	Pro	Gln	Phe	Glu	Gly	Gln	Thr	Lys	Thr	Lys	
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Leu	Gly	Asn	Ser	Glu	Val	Ser	Gly	Ala	Val	Asn	Gln	Ala	Val	Gly	Glu	
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[illegible]

7

Tyr	Pro	Gly	Gly	Leu	Val	Asp	Phe	Val	Lys	His	Ile	Asn	Arg	Thr	Lys		
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				165					170					175			
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His	Glu	Val	Glu	Ile	Ala	Met	Gln	Trp	Asn	Gly	Gly	Tyr	Ser	Glu	Ser		
				180					185					190			
gtg	cac	acc	ttc	gcc	aac	acc	atc	aac	acc	cat	gag	ggc	ggc	acc	cac	624	
Val	His	Thr	Phe	Ala	Asn	Thr	Ile	Asn	Thr	His	Glu	Gly	Gly	Thr	His		
				195					200					205			
gag	gag	ggc	ttc	cgc	agc	gcg	ctg	acc	tcg	gtg	gtg	aac	aag	tac	gcc	672	
Glu	Glu	Gly	Phe	Arg	Ser	Ala	Leu	Thr	Ser	Val	Val	Asn	Lys	Tyr	Ala		
				210					215					220			
aaa	gac	aag	aag	ctg	ctc	aag	gac	aag	gat	ccc	aac	ctc	acc	ggc	gac	720	
Lys	Asp	Lys	Lys	Leu	Leu	Lys	Asp	Lys	Asp	Pro	Asn	Leu	Thr	Gly	Asp		
225				230					235					240			
gac	atc	cga	gaa	ggg	ctg	gcc	gcg	gtg	atc	tcc	gtg	aag	gtc	gcc	gag	768	
Asp	Ile	Arg	Glu	Gly	Leu	Ala	Ala	Val	Ile	Ser	Val	Lys	Val	Ala	Glu		
				245					250					255			
ccg	cag	ttc	gag	ggc	cag	act	aag	acg	aaa	ctc	ggc	aac	acc	gag	gtc	816	
Pro	Gln	Phe	Glu	Gly	Gln	Thr	Lys	Thr	Lys	Leu	Gly	Asn	Thr	Glu	Val		
				260					265					270			
aag	tcg	ttt	gtc	cag	aaa	gtc	tgt	aac	gaa	caa	ctc	act	cac	tgg	ttc	864	
Lys	Ser	Phe	Val	Gln	Lys	Val	Cys	Asn	Glu	Gln	Leu	Thr	His	Trp	Phe		
				275					280					285			
gag	gcg	aac	ccg	tcg	gaa	gct	aaa	acc	gtt	gta	aac	aag	gcg	gtt	tcg	912	
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<213> Mycobacterium simiae

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35 40 45
Thr Leu Lys Gln Gly Glu Ala Thr Lys Lys Thr Gly Thr Thr Ile Arg
50 55 60
Phe Trp Ala Asp Pro Glu Ile Phe Glu Thr Thr Gln Tyr Asp Phe Glu
65 70 75 80
Thr Val Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu
85 90 95
Thr Ile Asn Leu Thr Asp Glu Arg Val Glu Gln Asp Glu Val Val Asp
100 105 110
Glu Val Val Ser Asp Thr Ala Glu Ala Pro Lys Ser Ala Glu Glu Gln
115 120 125
Ala Ala Glu Ser Ala Lys Pro His Lys Val Lys His Arg Thr Phe His
130 135 140
Tyr Pro Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys
145 150 155 160
Asn Pro Ile Gln Gln Ser Val Ile Asp Phe Asp Gly Lys Gly Thr Gly
165 170 175
His Glu Val Glu Ile Ala Met Gln Trp Asn Gly Gly Tyr Ser Glu Ser
180 185 190
Val His Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His
195 200 205
Glu Glu Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala

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210	215	220	
Lys Asp Lys Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp			
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Asp Ile Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ala Glu			
	245	250	255
Pro Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val			
	260	265	270
Lys Ser Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe			
	275	280	285
Glu Ala Asn Pro Ser Glu Ala Lys Thr Val Val Asn Lys Ala Val Ser			
	290	295	300
Ser Ala Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg			
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Arg Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp			
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Cys Arg Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly			
	340	345	350
Asp Ser Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln			
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Ala Ile Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg			
	370	375	380
Ile Asp Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala			
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Leu Gly Thr Gly Ile His Asp Glu Phe Asp Ile Thr Lys Leu Arg Tyr			
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His Lys Ile Val Leu			
	420		

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115	120	125	
tgc tct gaa aat gat cct gaa aaa tgt gaa ctg tac ctg gta gag ggt	432		
Cys Ser Glu Asn Asp Pro Glu Lys Cys Glu Leu Tyr Leu Val Glu Gly			
130	135	140	
gac tcc gca ggt ggt acg gct aaa caa gga cgt aac cgt agc ttc cag	480		
Asp Ser Ala Gly Gly Thr Ala Lys Gln Gly Arg Asn Arg Ser Phe Gln			
145	150	155	160
gcg atc ctg ccg ctc agg ggt aaa atc ctg aac gtg gag aaa gcc atg	528		
Ala Ile Leu Pro Leu Arg Gly Lys Ile Leu Asn Val Glu Lys Ala Met			
165	170	175	
gag cat aag ata tat gag aat gag gag att aaa aac atc ttc acc gca	576		
Glu His Lys Ile Tyr Glu Asn Glu Glu Ile Lys Asn Ile Phe Thr Ala			
180	185	190	
ctt ggt gta acc atc ggt acg gaa gaa gat gac aaa gcc ctc aac ctc	624		
Leu Gly Val Thr Ile Gly Thr Glu Glu Asp Asp Lys Ala Leu Asn Leu			
195	200	205	
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210	215	220	

<210> 6

<211> 220

<212> PRT

<213> Chitinophaga pinensis

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Asp	Phe	Arg	Glu	Gly	Leu	Ser	Ala	Ile	Ile	Ser	Val	Lys	Val	Pro	Glu
			35					40				45			
Pro	Gln	Phe	Glu	Gly	Gln	Thr	Lys	Thr	Lys	Leu	Gly	Asn	Ser	Asp	Val
			50				55				60				
Met	Gly	Val	Val	Asp	Ser	Ser	Val	Ala	Ala	Val	Leu	Asp	Ala	Tyr	Leu
65					70					75				80	
Glu	Glu	His	Pro	Arg	Glu	Ala	Lys	Ile	Ile	Ile	Asn	Lys	Val	Val	Leu
				85					90					95	
Ala	Ala	Gln	Ala	Arg	Glu	Ala	Ala	Arg	Lys	Ala	Arg	Gln	Met	Val	Gln
			100					105				110			
Arg	Lys	Ser	Val	Leu	Ser	Gly	Ser	Gly	Leu	Pro	Gly	Lys	Leu	Ala	Asp
		115					120				125				
Cys	Ser	Glu	Asn	Asp	Pro	Glu	Lys	Cys	Glu	Leu	Tyr	Leu	Val	Glu	Gly
	130					135				140					
Asp	Ser	Ala	Gly	Gly	Thr	Ala	Lys	Gln	Gly	Arg	Asn	Arg	Ser	Phe	Gln
145				150						155				160	
Ala	Ile	Leu	Pro	Leu	Arg	Gly	Lys	Ile	Leu	Asn	Val	Glu	Lys	Ala	Met
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Glu	His	Lys	Ile	Tyr	Glu	Asn	Glu	Glu	Ile	Lys	Asn	Ile	Phe	Thr	Ala
		180						185				190			
Leu	Gly	Val	Thr	Ile	Gly	Thr	Glu	Glu	Asp	Asp	Lys	Ala	Leu	Asn	Leu
		195					200				205				
Ser	Lys	Leu	Arg	Tyr	His	Lys	Leu	Ile	Ile	Met	Thr				
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<210> 7

<211> 537

<212> DNA

<213> *Flavobacterium aquatile*

<220>

<221> CDS

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Ser Cys Val Asn Ala Leu Ser Asp Asn Leu Lys Ala Thr Val Phe Arg
20 25 30
gac gga aaa gtg tac gag caa gaa tat gaa aaa ggt aaa gca atg tat 144
Asp Gly Lys Val Tyr Glu Gln Glu Tyr Glu Lys Gly Lys Ala Met Tyr
35 40 45
ccg gtt aag caa gtt ggt gaa aca aca aag cga gga aca atg gtt act 192
Pro Val Lys Gln Val Gly Glu Thr Thr Lys Arg Gly Thr Met Val Thr
50 55 60
ttt cat cct gat aaa acc att ttt act caa aca att gag tat tct tat 240
Phe His Pro Asp Lys Thr Ile Phe Thr Gln Thr Ile Glu Tyr Ser Tyr
65 70 75 80
gat aca ctt gca gca cgt atg cgt gaa tta tct ttc ctg aat aaa gga 288
Asp Thr Leu Ala Ala Arg Met Arg Glu Leu Ser Phe Leu Asn Lys Gly
85 90 95
att aca atc aca ctt aca gat aaa aga cat act aaa gac aac ggc gat 336

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Ile Thr Ile Thr Leu Thr Asp Lys Arg His Thr Lys Asp Asn Gly Asp
      100              105              110
ttt gaa ggt gaa gtt ttt cat tct aaa gaa ggg ctt aaa gaa ttc gtt 384
Phe Glu Gly Glu Val Phe His Ser Lys Glu Gly Leu Lys Glu Phe Val
      115              120              125
cga ttt tta gat gct ggt aga gaa cca att att tct cac gta ata agc 432
Arg Phe Leu Asp Ala Gly Arg Glu Pro Ile Ile Ser His Val Ile Ser
      130              135              140
atg gag cac gaa aaa gga gaa gtt cct gtt gag gtt gct ctt gtt tac 480
Met Glu His Glu Lys Gly Glu Val Pro Val Glu Val Ala Leu Val Tyr
      145              150              155              160
aal aca agt tac tcc gaa aat att ttc tct tac gta aat aat att aac 528
Asn Thr Ser Tyr Ser Glu Asn Ile Phe Ser Tyr Val Asn Asn Ile Asn
      165              170              175
acg cac gaa 537
Thr His Glu

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<210> 8

<211> 179

<212> PRT

<213> Flavobacterium aquatile

<400> 8

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Asp Gly Lys Val Tyr Glu Gln Glu Tyr Glu Lys Gly Lys Ala Met Tyr
      35              40              45

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Gly Glu Asn Ser Gly Tyr Thr Val Ser Gly Gly Leu His Gly Val Gly
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Val Ser Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Thr Ile Lys
20 25 30
cgc gac ggg cac gag tgg ttt cag tac tac gac cgc gcc gtg ccc gga 144
Arg Asp Gly His Glu Trp Phe Gln Tyr Tyr Asp Arg Ala Val Pro Gly
35 40 45
acc ctc aag cag ggc gag gcc acc aag aag acc gga acc acg atc agg 192
Thr Leu Lys Gln Gly Glu Ala Thr Lys Lys Thr Gly Thr Thr Ile Arg
50 55 60
ttc tgg gcg gac ccc gaa atc ttc gaa acc aca cag tac gac ttc gag 240
Phe Trp Ala Asp Pro Glu Ile Phe Glu Thr Thr Gln Tyr Asp Phe Glu
65 70 75 80
acc gtg gcg cgg cgg ctg cag gag atg gcc ttc ctc aac aag ggc ctc 288
Thr Val Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu
85 90 95
acc atc aac ctc acc gac gaa cga gtg gag cag gac gag gtc gtc gac 336
Thr Ile Asn Leu Thr Asp Glu Arg Val Glu Gln Asp Glu Val Val Asp
100 105 110
gag gtc gtc agc gac acc gcc gag gca ccg aag tcc gcc gaa gag aag 384
Glu Val Val Ser Asp Thr Ala Glu Ala Pro Lys Ser Ala Glu Glu Lys
115 120 125
gcc gcg gaa tgg act gcg cca cac aag gtc aag cac cgc acc ttc cac 432
Ala Ala Glu Ser Thr Ala Pro His Lys Val Lys His Arg Thr Phe His
130 135 140
tac ccc ggc ggt ctg gtc gac ttc gtc aag cac atc aac cgc acc aag 480
Tyr Pro Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys

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Gly	Glu	Asn	Ser	Gly	Tyr	Thr	Val	Ser	Gly	Gly	Leu	His	Gly	Val	Gly
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				20					25				30		
Arg	Asp	Gly	His	Glu	Trp	Phe	Gln	Tyr	Tyr	Asp	Arg	Ala	Val	Pro	Gly
				35					40				45		
Thr	Leu	Lys	Gln	Gly	Glu	Ala	Thr	Lys	Lys	Thr	Gly	Thr	Thr	Ile	Arg
				50					55				60		
Phe	Trp	Ala	Asp	Pro	Glu	Ile	Phe	Glu	Thr	Thr	Gln	Tyr	Asp	Phe	Glu
65					70						75				80
Thr	Val	Ala	Arg	Arg	Leu	Gln	Glu	Met	Ala	Phe	Leu	Asn	Lys	Gly	Leu
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Thr	Ile	Asn	Leu	Thr	Asp	Glu	Arg	Val	Glu	Gln	Asp	Glu	Val	Val	Asp
				100						105				110	
Glu	Val	Val	Ser	Asp	Thr	Ala	Glu	Ala	Pro	Lys	Ser	Ala	Glu	Glu	Lys
				115									120		125
Ala	Ala	Glu	Ser	Thr	Ala	Pro	His	Lys	Val	Lys	His	Arg	Thr	Phe	His
				130									135		140
Tyr	Pro	Gly	Gly	Leu	Val	Asp	Phe	Val	Lys	His	Ile	Asn	Arg	Thr	Lys
145					150						155				160
Ser	Pro	Ile	Gln	Gln	Ser	Val	Ile	Asp	Phe	Asp	Gly	Lys	Gly	Thr	Gly
				165							170				175
His	Glu	Val	Glu	Ile	Ala	Met	Gln	Trp	Asn	Gly	Gly	Tyr	Ser	Glu	Ser
				180									185		190
Val	His	Thr	Phe	Ala	Asn	Thr	Ile	Asn	Thr	His	Glu	Gly	Gly	Thr	His
				195									200		205
Glu	Glu	Gly	Phe	Arg	Ser	Ala	Leu	Thr	Ser	Val	Val	Asn	Lys	Tyr	Ala
				210									215		220
Lys	Asp	Lys	Lys	Leu	Leu	Lys	Asp	Lys	Asp	Pro	Asn	Leu	Thr	Gly	Asp

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23

Thr	Leu	Ala	Ser	Arg	Leu	Lys	Glu	Leu	Ala	Tyr	Leu	Asn	Ala	Gly	Val	
145					150					155					160	
cgc	atc	gac	ttt	acc	gat	gag	cgg	ctg	cag	ctc	acc	aag	aat	cac	gag	528
Arg	Ile	Asp	Phe	Thr	Asp	Glu	Arg	Leu	Gln	Leu	Thr	Lys	Asn	His	Glu	
					165					170					175	
ccc	cat	caa	gaa	acc	tat	tac	ttt	gaa	ggc	ggt	att	cgc	gaa	tac	gtc	576
Pro	His	Gln	Glu	Thr	Tyr	Tyr	Phe	Glu	Gly	Gly	Ile	Arg	Glu	Tyr	Val	
					180					185					190	
gcc	tac	atg	aat	acc	gat	aaa	cag	cgc	ctg	cac	tca	gag	att	atc	ttt	624
Ala	Tyr	Met	Asn	Thr	Asp	Lys	Gln	Ala	Leu	His	Ser	Glu	Ile	Ile	Phe	
					195					200					205	
gtg	caa	tcc	gaa	aaa	gat	ggc	gtc	caa	gtt	gaa	gct	gca	ttg	caa	tgg	672
Val	Gln	Ser	Glu	Lys	Asp	Gly	Val	Gln	Val	Glu	Ala	Ala	Leu	Gln	Trp	
					210					215					220	
tgc	gtt	gac	gcc	tac	agc	gac	aac	att	ctg	ggc	ttt	gcc	aac	aac	alc	720
Cys	Val	Asp	Ala	Tyr	Ser	Asp	Asn	Ile	Leu	Gly	Phe	Ala	Asn	Asn	Ile	
225					230					235					240	
cgc	acg	att	gac	ggc	ggc	acc	cat	att	gag	ggg	ctc	aaa	act	gtt	ctg	768
Arg	Thr	Ile	Asp	Gly	Gly	Thr	His	Ile	Glu	Gly	Leu	Lys	Thr	Val	Leu	
					245					250					255	
acg	cgg	acg	atg	aac	acg	atc	gcc	cgc	aaa	cgg	aat	aaa	cgc	aag	gat	816
Thr	Arg	Thr	Met	Asn	Thr	Ile	Ala	Arg	Lys	Arg	Asn	Lys	Arg	Lys	Asp	
					260					265					270	
gcc	gac	aat	aac	ctg	tcg	ggc	gag	aat	att	cgc	gaa	ggg	tta	aca	gcg	864
Ala	Asp	Asn	Asn	Leu	Ser	Gly	Glu	Asn	Ile	Arg	Glu	Gly	Leu	Thr	Ala	
					275					280					285	
atc	gtt	tcg	gtc	aaa	gtt	ccg	gat	ccg	gaa	ttt	gaa	ggg	caa	acc	aaa	912
Ile	Val	Ser	Val	Lys	Val	Pro	Asp	Pro	Glu	Phe	Glu	Gly	Gln	Thr	Lys	
290					295					300						

Gly Arg Gly Ile Pro Thr Asp Ile His Pro Gln Thr Gly Lys Ser Ala
 35 40 45
 Leu Glu Thr Val Leu Thr Ile Leu His Ala Gly Gly Lys Phe Gly Gly
 50 55 60
 Gly Gly Tyr Lys Val Ser Gly Gly Leu His Gly Val Gly Val Ser Val
 65 70 75 80
 Val Asn Ala Leu Ser Glu Tyr Val Glu Val Thr Val Trp Arg Glu Gly
 85 90 95
 Lys Thr His Gln Gln Arg Phe Glu Gln Gly Asn Pro Ile Gly Glu Leu
 100 105 110
 Gln Val Ala Pro Asp Ala Asp Asp Arg Arg Gly Thr Gln Val Arg Phe
 115 120 125
 Lys Pro Asp Ala Thr Ile Phe Ser Glu Thr Thr Glu Phe Asp Tyr Gly
 130 135 140
 Thr Leu Ala Ser Arg Leu Lys Glu Leu Ala Tyr Leu Asn Ala Gly Val
 145 150 155 160
 Arg Ile Asp Phe Thr Asp Glu Arg Leu Gln Leu Thr Lys Asn His Glu
 165 170 175
 Pro His Gln Glu Thr Tyr Tyr Phe Glu Gly Gly Ile Arg Glu Tyr Val
 180 185 190
 Ala Tyr Met Asn Thr Asp Lys Gln Ala Leu His Ser Glu Ile Ile Phe
 195 200 205
 Val Gln Ser Glu Lys Asp Gly Val Gln Val Glu Ala Ala Leu Gln Trp
 210 215 220
 Cys Val Asp Ala Tyr Ser Asp Asn Ile Leu Gly Phe Ala Asn Asn Ile
 225 230 235 240
 Arg Thr Ile Asp Gly Gly Thr His Ile Glu Gly Leu Lys Thr Val Leu
 245 250 255
 Thr Arg Thr Met Asn Thr Ile Ala Arg Lys Arg Asn Lys Arg Lys Asp

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260	265	270
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275	280	285
Ile Val Ser Val Lys Val Pro Asp Pro Glu Phe Glu Gly Gln Thr Lys		
290	295	300
Thr Lys Leu Gly Asn Thr Glu Val Arg Gly Ile Val Asp Thr Leu Val		
305	310	315
Gly Glu Thr Leu Thr Glu Tyr Leu Glu Phe His Pro Ser Val Ala Asp		
325	330	335
Leu Ile Leu Glu Lys Ala Ile Gln Ala Phe Asn Ala Ala Glu Ala Ala		
340	345	350
Arg Arg Ala Arg Glu Leu Val Arg Arg Lys Ser Val Leu Glu Ser Ser		
355	360	365
Thr Leu Pro Gly Lys Leu Ala Asp Cys Ser Ser Arg Asp Pro Gly Glu		
370	375	380
Ser Glu Ile Phe Ile Val		
385	390	

<210> 15

<211> 696

<212> DNA

<213> *Caulobacter crescentus*

<220>

<221> CDS

<222> (1)... (696)

<400> 15

cag aac agc tac aag gtc tcg ggc ggt ctg cac ggc gtg ggc gtc tcg 48

Gln	Asn	Ser	Tyr	Lys	Val	Ser	Gly	Gly	Leu	His	Gly	Val	Gly	Val	Ser	
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gtc	gtg	aac	gcc	ctg	tcg	gat	tgg	ctg	gag	ctg	ctg	atc	cac	cgc	aac	96
Val	Val	Asn	Ala	Leu	Ser	Asp	Trp	Leu	Glu	Leu	Leu	Ile	His	Arg	Asn	
				20					25					30		
ggc	aag	gtc	cac	cag	atg	cgc	ttc	gag	cgc	ggc	gac	gcg	gtc	acc	tcg	144
Gly	Lys	Val	His	Gln	Met	Arg	Phe	Glu	Arg	Gly	Asp	Ala	Val	Thr	Ser	
				35					40					45		
ctg	aag	gtc	acc	ggc	gac	tcg	ccc	gtg	cgg	acc	gag	ggc	ccc	aag	gcc	192
Leu	Lys	Val	Thr	Gly	Asp	Ser	Pro	Val	Arg	Thr	Glu	Gly	Pro	Lys	Ala	
				50					55					60		
ggc	gag	acc	ctg	acc	ggt	acg	gaa	gtt	acg	ttc	ttt	ccg	tcg	aag	gac	240
Gly	Glu	Thr	Leu	Thr	Gly	Thr	Glu	Val	Thr	Phe	Phe	Pro	Ser	Lys	Asp	
				65					70					75		
acc	ttc	gcc	ttc	atc	gaa	ttc	gac	cgg	aag	acg	ctg	gag	cac	cgc	ctg	288
Thr	Phe	Ala	Phe	Ile	Glu	Phe	Asp	Arg	Lys	Thr	Leu	Glu	His	Arg	Leu	
				85					90					95		
cgc	gag	ctg	gcc	ttc	ctg	aac	tcg	ggc	gtg	acg	atc	tgg	ttc	aag	gac	336
Arg	Glu	Leu	Ala	Phe	Leu	Asn	Ser	Gly	Val	Thr	Ile	Trp	Phe	Lys	Asp	
				100					105					110		
cat	cgc	gac	gtc	gag	ccg	tgg	gaa	gag	aag	ctg	ttc	tac	gag	ggc	ggc	384
His	Arg	Asp	Val	Glu	Pro	Trp	Glu	Glu	Lys	Leu	Phe	Tyr	Glu	Gly	Gly	
				115					120					125		
atc	gag	gcc	ttc	gtg	cgc	cac	ctc	gac	aag	gcc	aag	acg	ccg	ctg	ctg	432
Ile	Glu	Ala	Phe	Val	Arg	His	Leu	Asp	Lys	Ala	Lys	Thr	Pro	Leu	Leu	
				130					135					140		
aag	gcc	ccg	atc	gcc	gtc	aag	ggc	gtc	aag	gac	aag	gtc	gag	atc	gac	480
Lys	Ala	Pro	Ile	Ala	Val	Lys	Gly	Val	Lys	Asp	Lys	Val	Glu	Ile	Asp	
145									150					155		160

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<221> CDS

<222> (1)... (888)

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gag ctg gtc ctg acc gtt cgc cgt agc ggc aag atc tgg gaa cag acc 96

Glu Leu Val Leu Thr Val Arg Arg Ser Gly Lys Ile Trp Glu Gln Thr

20 25 30

tac gtc cat ggt gtt ccg cag gaa ccg atg aag atc gtt ggc gac agc 144

Tyr Val His Gly Val Pro Gln Glu Pro Met Lys Ile Val Gly Asp Ser

35 40 45

gaa acc acc ggc acc cag atc cac ttc aag gct tcc agc gaa acc ttc 192

Glu Thr Thr Gly Thr Gln Ile His Phe Lys Ala Ser Ser Glu Thr Phe

50 55 60

aag aac atc cac ttc agc tgg gac atc ctg gcc aag cgg att cgt gaa 240

Lys Asn Ile His Phe Ser Trp Asp Ile Leu Ala Lys Arg Ile Arg Glu

65 70 75 80

ctg tcc ttc ctg aac tcc ggt gtc ggc atc gtc ctg aag gat gag cgc 288

Leu Ser Phe Leu Asn Ser Gly Val Gly Ile Val Leu Lys Asp Glu Arg

85 90 95

agc ggc aag gaa gaa ctg ttc aag tac gaa ggc ggc ttg cgc gcg ttc 336

Ser Gly Lys Glu Glu Leu Phe Lys Tyr Glu Gly Gly Leu Arg Ala Phe

100 105 110

ggt gaa tac ctg aac acc aac aag acc ccg gtc aac cag gtg ttc cat 384

Val Glu Tyr Leu Asn Thr Asn Lys Thr Pro Val Asn Gln Val Phe His

115 120 125

ttc aac atc cag cgc gaa gac ggc atc ggc gta gaa atc gcc ctg cag	432
Phe Asn Ile Gln Arg Glu Asp Gly Ile Gly Val Glu Ile Ala Leu Gln	
130 135 140	
tgg aac gac agc ttc aac gag aac ctg ttg tgc ttc acc aac aac att	480
Trp Asn Asp Ser Phe Asn Glu Asn Leu Leu Cys Phe Thr Asn Asn Ile	
145 150 155 160	
ccg cag cgc gat ggc ggt acf cac ctg gtg ggt ttc cgt tcc gcc ctg	528
Pro Gln Arg Asp Gly Gly Thr His Leu Val Gly Phe Arg Ser Ala Leu	
165 170 175	
acg cgt aac ctc aat acg tat atc gaa gcc gaa ggc ctg gcg aag aag	576
Thr Arg Asn Leu Asn Thr Tyr Ile Glu Ala Glu Gly Leu Ala Lys Lys	
180 185 190	
cac aag gtc gcg acc acc ggt gac gat gcc cgt gaa ggc ctg gcc gcg	624
His Lys Val Ala Thr Thr Gly Asp Asp Ala Arg Glu Gly Leu Ala Ala	
195 200 205	
atc att tgc gta aaa gtg ccg gat ccg aag ttc agc tcc cag acc aag	672
Ile Ile Ser Val Lys Val Pro Asp Pro Lys Phe Ser Ser Gln Thr Lys	
210 215 220	
gac aag ctg gtt tct tcc gaa gtg aag acc gcg gtc gaa cag gaa atg	720
Asp Lys Leu Val Ser Ser Glu Val Lys Thr Ala Val Glu Gln Glu Met	
225 230 235 240	
ggc aag tac ttc tcc gac ttc ctg ctg gaa aac ccg aac gaa gcc aag	768
Gly Lys Tyr Phe Ser Asp Phe Leu Leu Glu Asn Pro Asn Glu Ala Lys	
245 250 255	
ctg gtt gtc ggc aag atg atc gac gcg gca cgt gct cgt gaa gcg gcg	816
Leu Val Val Gly Lys Met Ile Asp Ala Ala Arg Ala Arg Glu Ala Ala	
260 265 270	
cgc aag acc cgt gag atg acc cgc cgc aaa ggc gcg ctg gac atc gcc	864
Arg Lys Thr Arg Glu Met Thr Arg Arg Lys Gly Ala Leu Asp Ile Ala	

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275	280	285	
ggc ctg ccg ggc aaa ctg gct gac			888
Gly Leu Pro Gly Lys Leu Ala Asp			
290	295		
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<400> 18			
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20	25	30	
Tyr Val His Gly Val Pro Gln Glu Pro Met Lys Ile Val Gly Asp Ser			
35	40	45	
Glu Thr Thr Gly Thr Gln Ile His Phe Lys Ala Ser Ser Glu Thr Phe			
50	55	60	
Lys Asn Ile His Phe Ser Trp Asp Ile Leu Ala Lys Arg Ile Arg Glu			
65	70	75	80
Leu Ser Phe Leu Asn Ser Gly Val Gly Ile Val Leu Lys Asp Glu Arg			
85	90	95	
Ser Gly Lys Glu Glu Leu Phe Lys Tyr Glu Gly Gly Leu Arg Ala Phe			
100	105	110	
Val Glu Tyr Leu Asn Thr Asn Lys Thr Pro Val Asn Gln Val Phe His			
115	120	125	
Phe Asn Ile Gln Arg Glu Asp Gly Ile Gly Val Glu Ile Ala Leu Gln			
130	135	140	

Trp Asn Asp Ser Phe Asn Glu Asn Leu Leu Cys Phe Thr Asn Asn Ile
 145 150 155 160
 Pro Gln Arg Asp Gly Gly Thr His Leu Val Gly Phe Arg Ser Ala Leu
 165 170 175
 Thr Arg Asn Leu Asn Thr Tyr Ile Glu Ala Glu Gly Leu Ala Lys Lys
 180 185 190
 His Lys Val Ala Thr Thr Gly Asp Asp Ala Arg Glu Gly Leu Ala Ala
 195 200 205
 Ile Ile Ser Val Lys Val Pro Asp Pro Lys Phe Ser Ser Gln Thr Lys
 210 215 220
 Asp Lys Leu Val Ser Ser Glu Val Lys Thr Ala Val Glu Gln Glu Met
 225 230 235 240
 Gly Lys Tyr Phe Ser Asp Phe Leu Leu Glu Asn Pro Asn Glu Ala Lys
 245 250 255
 Leu Val Val Gly Lys Met Ile Asp Ala Ala Arg Ala Arg Glu Ala Ala
 260 265 270
 Arg Lys Thr Arg Glu Met Thr Arg Arg Lys Gly Ala Leu Asp Ile Ala
 275 280 285
 Gly Leu Pro Gly Lys Leu Ala Asp
 290 295

<210> 19

<211> 531

<212> DNA

<213> *Synechococcus* sp.

<220>

<221> CDS

<222> (1)... (531)

[illegible]

35

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 Arg Ser Leu Leu Glu Gln Gly Tyr Met Tyr Ile Ala Cys Pro Pro Leu
 130 135 140
 Tyr Lys Leu Glu Arg Gly Arg Asn His Tyr Tyr Cys Tyr Asn Glu Arg
 145 150 155 160
 Glu Leu Gln Glu Arg Ile Ala Thr Phe Pro Glu Asn Ala Asn Tyr Thr
 165 170 175
 Ile

<210> 21
 <211> 660
 <212> DNA
 <213> *Caulobacter crescentus*

<220>
 <221> CDS
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<400> 21
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 Arg Asp Gly Gly Thr His Leu Ser Ala Phe Arg Ala Ala Leu Thr Arg
 1 5 10 15
 atc atc acc agc tac gcc gag agc tcc ggc atc ctg aag aag gaa aag 96
 Ile Ile Thr Ser Tyr Ala Glu Ser Ser Gly Ile Leu Lys Lys Glu Lys
 20 25 30
 gtc agc ctg ggc ggc gaa gac agc cgc gag ggc ctg acc tgc gtg ctg 144
 Val Ser Leu Gly Gly Glu Asp Ser Arg Glu Gly Leu Thr Cys Val Leu
 35 40 45

tcg gtc aag gtc ccg gat ccg aag ttc agc tcg cag acc aag gac aag	192
Ser Val Lys Val Pro Asp Pro Lys Phe Ser Ser Gln Thr Lys Asp Lys	
50 55 60	
ctg gtc tcg tcc gaa gtc cgc ccc gcc gtt gag gcc ctg gtc tcg gaa	240
Leu Val Ser Ser Glu Val Arg Pro Ala Val Glu Gly Leu Val Ser Glu	
65 70 75 80	
ggc ctc tcg acc tgg ttc gag gaa cat ccg aac gag gcc aag gcg atc	288
Gly Leu Ser Thr Trp Phe Glu Glu His Pro Asn Glu Ala Lys Ala Ile	
85 90 95	
gtg acc aag atc gcc gag gcc gcc gcc gcc cgc gag gcc gcc cgc aag	336
Val Thr Lys Ile Ala Glu Ala Ala Ala Ala Arg Glu Ala Ala Arg Lys	
100 105 110	
gcg cga gag ctg acc cgc cgc aag agc gcg ctc gac atc acc agc ctg	384
Ala Arg Glu Leu Thr Arg Arg Lys Ser Ala Leu Asp Ile Thr Ser Leu	
115 120 125	
ccc gcc aag ctc gcc gac tgc tcg gaa cgc gat ccg gcc aag tcc gag	432
Pro Gly Lys Leu Ala Asp Cys Ser Glu Arg Asp Pro Ala Lys Ser Glu	
130 135 140	
atc ttc atc gtc gag gcc gac tcg gcg gcc gcc tcg gcc aag cag gcc	480
Ile Phe Ile Val Glu Gly Asp Ser Ala Gly Gly Ser Ala Lys Gln Ala	
145 150 155 160	
cgc aac cgc gac aac cag gcc gtt ctg ccc ctg cgc gcc aag atc ctg	528
Arg Asn Arg Asp Asn Gln Ala Val Leu Pro Leu Arg Gly Lys Ile Leu	
165 170 175	
aac gtc gag cgg gcc cgc ttc gac aag atg ctg tcg tcc gac cag atc	576
Asn Val Glu Arg Ala Arg Phe Asp Lys Met Leu Ser Ser Asp Gln Ile	
180 185 190	
ggc acg ctg atc acc gcc ctg gcc gcg ggg atc gcc cgc gac gac ttc	624
Gly Thr Leu Ile Thr Ala Leu Gly Ala Gly Ile Gly Arg Asp Asp Phe	

35	40	45	
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Pro Val Lys Ser Ile Gly Glu Thr Glu Glu Thr Gly Thr Ile Val Thr			
50	55	60	
ttt tac cca gat gat act ata ttt aca caa act aca gag tat aat tat			240
Phe Tyr Pro Asp Asp Thr Ile Phe Thr Gln Thr Thr Glu Tyr Asn Tyr			
65	70	75	80
gaa acg ctt tct aac aga atg cga gag ttg gct tac ctt aat aag gga			288
Glu Thr Leu Ser Asn Arg Met Arg Glu Leu Ala Tyr Leu Asn Lys Gly			
85	90	95	
gtt aca att agc att aca gat aag aga gtt aaa gat gaa aag gga gag			336
Val Thr Ile Ser Ile Thr Asp Lys Arg Val Lys Asp Glu Lys Gly Glu			
100	105	110	
ttt tta tct gaa gtt ttt tac tct gaa gaa gga cta aaa gaa ttt att			384
Phe Leu Ser Glu Val Phe Tyr Ser Glu Glu Gly Leu Lys Glu Phe Ile			
115	120	125	
aag ttt tta gac ggt aac aga gaa caa cta ata cgt gat gtt gtt tca			432
Lys Phe Leu Asp Gly Asn Arg Glu Gln Leu Ile Arg Asp Val Val Ser			
130	135	140	
atg gaa ggt gaa aaa aac gga att cct gtt gag gtt gca atg gtg tac			480
Met Glu Gly Glu Lys Asn Gly Ile Pro Val Glu Val Ala Met Val Tyr			
145	150	155	160
aat aca tca tat tca gaa aat ctt cac tct tac gta aat aat att aat			528
Asn Thr Ser Tyr Ser Glu Asn Leu His Ser Tyr Val Asn Asn Ile Asn			
165	170	175	
aca cat gaa ggt ggt aca cac ctt tca ggt ttt aga aga ggt tta aca			576
Thr His Glu Gly Gly Thr His Leu Ser Gly Phe Arg Arg Gly Leu Thr			
180	185	190	
tca acc tta aaa aag tat gca gat gca tct gga atg tta gac aaa tta			624

Ser Thr Leu Lys Lys Tyr Ala Asp Ala Ser Gly Met Leu Asp Lys Leu	
195	200
aag ttt gag att cag gga gat gat ttt aga gaa ggt tta acg gct att	672
Lys Phe Glu Ile Gln Gly Asp Asp Phe Arg Glu Gly Leu Thr Ala Ile	
210	215
gtg tct gtt aaa gtt gca gaa cct cag ttt gaa ggg caa aca aaa act	720
Val Ser Val Lys Val Ala Glu Pro Gln Phe Glu Gly Gln Thr Lys Thr	
225	230
aaa tta ggt aac aga gaa gtt tct tct gca gtg agc caa gct gta tca	768
Lys Leu Gly Asn Arg Glu Val Ser Ser Ala Val Ser Gln Ala Val Ser	
245	250
gaa atg ctt acc aac tat tta gaa gaa aac cca gat gat gct aag gta	816
Glu Met Leu Thr Asn Tyr Leu Glu Glu Asn Pro Asp Asp Ala Lys Val	
260	265
att gta caa aaa gtc att ttg gca gcg caa gca cgt cat gcg gct aca	864
Ile Val Gln Lys Val Ile Leu Ala Ala Gln Ala Arg His Ala Ala Thr	
275	280
aaa gcc cgt gaa atg gta cag cgt aaa acg gta atg agt ata ggt ggt	912
Lys Ala Arg Glu Met Val Gln Arg Lys Thr Val Met Ser Ile Gly Gly	
290	295
tta cca ggg aaa tta tca gac tgt tct gag caa gat gct aca aaa tgc	960
Leu Pro Gly Lys Leu Ser Asp Cys Ser Glu Gln Asp Ala Thr Lys Cys	
305	310
gaa gta ttc ctt gta gag gga gat tcg gcg ggt ggt act gct aaa caa	1008
Glu Val Phe Leu Val Glu Gly Asp Ser Ala Gly Gly Thr Ala Lys Gln	
325	330
ggt agg gac aga aac ttt cag gca ata tta ccg ctt cgt ggt aaa atc	1056
Gly Arg Asp Arg Asn Phe Gln Ala Ile Leu Pro Leu Arg Gly Lys Ile	
340	345
	350

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tta aat gtt gaa aaa gca atg caa cat aag gtt ttt gaa aac gaa gaa 1104
Leu Asn Val Glu Lys Ala Met Gln His Lys Val Phe Glu Asn Glu Glu
      355              360              365

ata aaa aat att tac aca gct tta ggt gtt act att ggt aca gaa gaa 1152
Ile Lys Asn Ile Tyr Thr Ala Leu Gly Val Thr Ile Gly Thr Glu Glu
      370              375              380

gat agt aaa gcc tta aac tta gaa aaa tta aga tac cat aaa gta gtt 1200
Asp Ser Lys Ala Leu Asn Leu Glu Lys Leu Arg Tyr His Lys Val Val
      385              390              395              400

att atg tgt gat gcc gat gta gat ggt agc cac att gaa act tta atc 1248
Ile Met Cys Asp Ala Asp Val Asp Gly Ser His Ile Glu Thr Leu Ile
      405              410              415

ctt aca ttc ttc ttc cgt ttt atg agg gag tta ata gaa ggc ggt cac 1296
Leu Thr Phe Phe Phe Arg Phe Met Arg Glu Leu Ile Glu Gly Gly His
      420              425              430

gtt tat ata gca acc cca cct tta tac ttg gta aaa aag gga aca aaa 1344
Val Tyr Ile Ala Thr Pro Pro Leu Tyr Leu Val Lys Lys Gly Thr Lys
      435              440              445

aaa cgt tat gct tgg aat gat aaa gaa cga gat gag ata gca gaa agc 1392
Lys Arg Tyr Ala Trp Asn Asp Lys Glu Arg Asp Glu Ile Ala Glu Ser
      450              455              460

ttt aat ggt agt gtt ggt ata caa aga tat 1422
Phe Asn Gly Ser Val Gly Ile Gln Arg Tyr
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<211> 474

<212> PRT

<213> Cytophaga lytica

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<400> 24

Asp	Lys	Asp	Ser	Tyr	Lys	Val	Ser	Gly	Gly	Leu	His	Gly	Val	Gly	Val
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			20						25					30	
Glu	Gly	Lys	Ile	Trp	Glu	Gln	Glu	Tyr	Glu	Arg	Gly	Lys	Ala	Leu	Tyr
			35						40					45	
Pro	Val	Lys	Ser	Ile	Gly	Glu	Thr	Glu	Glu	Thr	Gly	Thr	Ile	Val	Thr
			50						55					60	
Phe	Tyr	Pro	Asp	Asp	Thr	Ile	Phe	Thr	Gln	Thr	Thr	Glu	Tyr	Asn	Tyr
			65						70					75	
Glu	Thr	Leu	Ser	Asn	Arg	Met	Arg	Glu	Leu	Ala	Tyr	Leu	Asn	Lys	Gly
									85					90	
Val	Thr	Ile	Ser	Ile	Thr	Asp	Lys	Arg	Val	Lys	Asp	Glu	Lys	Gly	Glu
									100					105	
Phe	Leu	Ser	Glu	Val	Phe	Tyr	Ser	Glu	Glu	Gly	Leu	Lys	Glu	Phe	Ile
									115					120	
Lys	Phe	Leu	Asp	Gly	Asn	Arg	Glu	Gln	Leu	Ile	Arg	Asp	Val	Val	Ser
									130					135	
Met	Glu	Gly	Glu	Lys	Asn	Gly	Ile	Pro	Val	Glu	Val	Ala	Met	Val	Tyr
									145					150	
Asn	Thr	Ser	Tyr	Ser	Glu	Asn	Leu	His	Ser	Tyr	Val	Asn	Asn	Ile	Asn
														165	
Thr	His	Glu	Gly	Gly	Thr	His	Leu	Ser	Gly	Phe	Arg	Arg	Gly	Leu	Thr
									170					175	
Ser	Thr	Leu	Lys	Lys	Tyr	Ala	Asp	Ala	Ser	Gly	Met	Leu	Asp	Lys	Leu
									180					185	
Ser	Thr	Leu	Lys	Lys	Tyr	Ala	Asp	Ala	Ser	Gly	Met	Leu	Asp	Lys	Leu
									195					200	
Lys	Phe	Glu	Ile	Gln	Gly	Asp	Asp	Phe	Arg	Glu	Gly	Leu	Thr	Ala	Ile

210					215					220									
Val	Ser	Val	Lys	Val	Ala	Glu	Pro	Gln	Phe	Glu	Gly	Gln	Thr	Lys	Thr				
225					230					235					240				
Lys	Leu	Gly	Asn	Arg	Glu	Val	Ser	Ser	Ala	Val	Ser	Gln	Ala	Val	Ser				
245					250					255									
Glu	Met	Leu	Thr	Asn	Tyr	Leu	Glu	Glu	Asn	Pro	Asp	Asp	Ala	Lys	Val				
260					265					270									
Ile	Val	Gln	Lys	Val	Ile	Leu	Ala	Ala	Gln	Ala	Arg	His	Ala	Ala	Thr				
275					280					285									
Lys	Ala	Arg	Glu	Met	Val	Gln	Arg	Lys	Thr	Val	Met	Ser	Ile	Gly	Gly				
290					295					300									
Leu	Pro	Gly	Lys	Leu	Ser	Asp	Cys	Ser	Glu	Gln	Asp	Ala	Thr	Lys	Cys				
305					310					315					320				
Glu	Val	Phe	Leu	Val	Glu	Gly	Asp	Ser	Ala	Gly	Gly	Thr	Ala	Lys	Gln				
325					330					335									
Gly	Arg	Asp	Arg	Asn	Phe	Gln	Ala	Ile	Leu	Pro	Leu	Arg	Gly	Lys	Ile				
340					345					350									
Leu	Asn	Val	Glu	Lys	Ala	Met	Gln	His	Lys	Val	Phe	Glu	Asn	Glu	Glu				
355					360					365									
Ile	Lys	Asn	Ile	Tyr	Thr	Ala	Leu	Gly	Val	Thr	Ile	Gly	Thr	Glu	Glu				
370					375					380									
Asp	Ser	Lys	Ala	Leu	Asn	Leu	Glu	Lys	Leu	Arg	Tyr	His	Lys	Val	Val				
385					390					395					400				
Ile	Met	Cys	Asp	Ala	Asp	Val	Asp	Gly	Ser	His	Ile	Glu	Thr	Leu	Ile				
405					410					415									
Leu	Thr	Phe	Phe	Phe	Arg	Phe	Met	Arg	Glu	Leu	Ile	Glu	Gly	Gly	His				
420					425					430									
Val	Tyr	Ile	Ala	Thr	Pro	Pro	Leu	Tyr	Leu	Val	Lys	Lys	Gly	Thr	Lys				
435					440					445									

Lys Arg Tyr Ala Trp Asn Asp Lys Glu Arg Asp Glu Ile Ala Glu Ser

450

455

460

Phe Asn Gly Ser Val Gly Ile Gln Arg Tyr

465

470

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<213> Artificial Sequence

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<210> 26

<211> 7

<212> DNA

<213> Artificial Sequence

<400> 26

His Ala Gly Gly Lys Phe Asp

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<210> 27

<211> 36

<212> DNA

<213> Artificial Sequence

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cicggttcgt atatgagenc cricnacric ngeric

36

<210> 28

<211> 12

<212> PRT

<213> Artificial Sequence

<400> 28

Asp Ala Asp Val Asp Gly Ala His Ile Arg Thr Leu

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<210> 29

<211> 41

<212> DNA

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<210> 30

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03-07-2016

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<212> PRT

<213> Artificial Sequence

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Lys Arg Pro Ala Met Tyr Ile Gly

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<211> 8

<212> PRT

<213> Artificial Sequence

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Lys Arg Pro Gly Met Tyr Ile Gly

1 5

<400> 51

Gln Leu Trp Glu Thr Thr Met

1 5

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<213> Artificial Sequence

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Gln Leu Trp Asp Thr Thr Met

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<211> 41

<212> DNA

<213> Artificial Sequence

<400> 53

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<210> 54

<211> 14

<212> PRT

<213> Artificial Sequence

<400> 54

Glu Val Ile Met Thr Val Leu His Ala Gly Gly Lys Phe Asp

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<210> 55

<211> 14

<212> PRT

<213> Artificial Sequence

<400> 55

Glu Val Ile Met Thr Val Leu His Ala Gly Gly Lys Phe Asn

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<210> 56

<211> 14

<212> PRT

<213> Artificial Sequence

<400> 56

Glu Val Ile Met Thr Val Leu His Ala Gly Gly Lys Phe Glu

1 5 10

<210> 57

<211> 14

<212> PRT

<213> Artificial Sequence

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Glu Val Ile Met Thr Val Leu His Ala Gly Gly Lys Phe Lys

1 5 10

<400> 61

Thr Asn Asn Ile Pro Gln

1 5

<210> 62

<211> 38

<212> DNA

<213> Artificial Sequence

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tgtaaaacga cggccagtaa ytinggnctn ggnacytt

38

<210> 63

<211> 7

<212> PRT

<213> Artificial Sequence

<400> 63

Lys Val Pro Asp Pro Lys Phe

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<210> 64

<211> 7

<212> PRT

<213> Artificial Sequence

<400> 64

Lys Val Pro Glu Pro Lys Phe

1

5

<210> 65

<211> 35

<212> DNA

<213> Artificial Sequence

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caggaaacag ctatgaccgc nmrnmrngcn mgnga

35

<210> 66

<211> 6

<212> PRT

<213> Artificial Sequence

<400> 66

Ala Arg Arg Ala Arg Glu

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<210> 67

<211> 6

<212> PRT

<213> Artificial Sequence

<400> 67

Ala Arg Lys Ala Arg Glu

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<211> 6

<212> PRT

<213> Artificial Sequence

<400> 68

Ala Lys Lys Ala Arg Glu

1 5

<210> 69

<211> 19

<212> PRT

<213> Artificial Sequence

<223> Xaa1 = Pro or Ser; Xaa2 = Ala or Thr; Xaa3 = Ala, Val or Leu; Xaa4 = Glu or Asp;

Xaa5 = Val or Thr; Xaa6 = Ile or Val; Xaa7 = Met, Leu or Phe; Xaa8 = Val, Gln or Ile;

Xaa9 = Asp or Gly; Xaa10 = Asp, Gly, Asn or Ser; Xaa11 = Ser, Lys, Gly, Asp or Asn

<400> 69

Xaa Xaa Xaa Xaa Xaa Xaa Thr Xaa Leu His Ala Gly Gly Lys Phe

1 5 10 15

Xaa Xaa Xaa

<210> 70

<211> 4

<212> PRT

<213> Artificial Sequence

<400> 70

Gly Gly Thr His

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<210> 71

<211> 15

<212> PRT

<213> Artificial Sequence

<223> Xaa1 = Ile or Leu; Xaa2 = Ala or Ser

<400> 71

Xaa Met Thr Asp Ala Asp Val Asp Gly Xaa His Ile Arg Thr Leu

1 5 10 15

<210> 72

<211> 11

<212> PRT

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<223> Xaa1 = Gly or Ala; Xaa2 = Ser or Asp

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Arg Lys Arg Pro Xaa Met Tyr Ile Gly Xaa Thr

1 5 10

<210> 73

<211> 6

<212> PRT

<213> Artificial Sequence

<223> Xaa1 = Thr or Pro; Xaa2 = Lys or Asn; Xaa3 = Thr, Asp, Gly, Lys, Ser, Phe or Tyr

<400> 73

Gln Xaa Xaa Xaa Lys Leu

1 5

<210> 74
 <211> 9
 <212> PRT
 <213> Artificial Sequence
 <223> Xaa1 = Tyr or Phe; Xaa2 = Ala or Pro

<400> 74
 Xaa Lys Gly Leu Gly Glu Met Asn Xaa
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<210> 75
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<400> 75
 Val Glu Gly Asp Ser Ala Gly Gly Ser
 1 5

<210> 76
 <211> 7
 <212> PRT
 <213> Artificial Sequence
 <223> Xaa1 = His or Val; Xaa2 = Gln or Lys

<400> 76
 Lys Xaa Pro Asp Pro Xaa Phe
 1 5

<210> 77

<211> 14

<212> PRT

<213> Artificial Sequence

<223> Xaa1 = Ser or Gln; Xaa2 = Ser or Glu; Xaa3 = Lys or Arg; Xaa4 = Ala or Ser

<400> 77

Leu Pro Gly Lys Leu Ala Asp Cys Xaa Xaa Xaa Asp Pro Xaa

1

5

10

<210> 78

<211> 9

<212> PRT

<213> Artificial Sequence

<223> Xaa1 = Trp or Arg; Xaa2 = Glu or Asp; Xaa3 = Met or Leu; Xaa4 = Asp or Asn

<400> 78

Gln Leu Xaa Xaa Thr Thr Xaa Xaa Pro

1

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<210> 79

<211> 6

<212> PRT

<213> Artificial Sequence

<223> Xaa1 = Lys or Arg; Xaa2 = Lys or Arg

<400> 79

Ala Xaa Xaa Ala Arg Glu

1

5

<210> 80

<211> 7

<212> PRT

〈213〉 Artificial Sequence

<223> Xaa1 = Pro or Asn; Xaa2 = Thr or Gln

<400> 80

Phe Thr Asn Asn Ile Xaa Xaa

1 5

[illegible]